Material and Methods: Reservoir hosts of ZCL were captured by live trap. Rodent species were identified. Smear of each ears were prepared by scratching ears. Serous from rodent ears were isolated; then, inoculated to NNN, injected to susceptible animal. Slides were prepared to find *Leishmania* using microscope. DNAs were extracted by ISH Horovize method and gene was amplified by Nested PCR.
Results: 122 rodents were trapped from 8 study regions. 98 *Meriones lybicus*, 13 *Meriones persicus*, 4 *Rhombomis opimus* and one *Rattus rattus* were trapped. 6 rodents were not identified. *Leishmania* infections were found in *M. lybicus and M. persicus* using direct smear, inoculation in Balb/C and in NNN medium. Detection of *Leishmania major* in those rodents was confirmed molecularly.
Discussion: Based on finding and abundant of *M. lybicus*, high *Leishmania* infection in this rodent is the main reservoir of *Leishmania major* in Fars province. *M. persicus* is second reservoir host of ZCL. Fars province is one of new focus of endemic of lesihmaniasis in Iran.

PP-200 First detection of *Leishmania* parasite in *Meriones lybicus* reservoir of Zoonotic Cutaneous Leishmaniasis in Turkemen Sahara (Golastan province)

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Introduction: Zoonotic Cutaneous Leishmaniasis (ZCL) is a disease for which rodent's family Gerbilidae are reservoirs and Phlebotominae sand-flies are vectors. Turkemen Sahara is one of the endemic disease foci in Iran. Based on previous reports, the only reservoir of ZCL is *Rhombomis opimus*. For this, detection of *Leishmania* parasite in *M. libycus* was considered.
Material and Methods: Rodents of reservoir host of ZCL disease were captured by live trap. Serous from rodent ears were isolated; then, slide were prepared, inoculated to NNN, injected to susceptible animal to find *Leishmania* parasite. For confirming certain *Leishmania* parasite in rodents, DNA were extracted, kDNA and ITS-rDNA genes were used by semi-nested and nested PCR.
Results: 19 rodents were trapped from 8 study regions. *Leishmania major* infection detected in *M. lybicus* by both routine laboratory and molecular tools. After sequencing and comparing kDNA and ITS-rDNA genes with those in GenBank, *Leishmania major* in this rodent for first time confirmed certainly.
Discussion: Based on certain confirmation of *Leishmania major* in *M. lybicus*, this rodent should be considered as second reservoir of ZCL, however *R. opimus* is the main reservoir of ZCL in this region. In addition of routine laboratory methods, new molecular methods should be used to detect parasite in reservoirs host of ZCL.

PP-201 A2 gene among isolates from Iranian cutaneous leishmania species is highly conserved gene

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Objective: *Leishmania* are leading to broad spectrum of diseases, collectively known as leishmaniasis. The A2 gene/protein family could be one of the most eligible candidate factors of virulence in visceral leishmaniasis (VL) infections. The previous results confirmed that in *L. infantum*, several A2 proteins are abundantly expressed by the amastigote, but not by promastigote stage. As there are no data available on the pattern of A2 gene/protein in Iranian *Leishmania* isolates of cutaneous leishmaniasis (CL), the current study aimed to investigate molecular analysis of A2 proteins among *Leishmania* species.
Methods: An A2 gene was identified by sequencing from crude PCR products of 20 samples from Iranian CL patients.
Result: The results indicated the A2 gene in CL is a single copy of only 153 bp encoding for a protein of 51 amino acids, as opposed to A2 of VL species that are multi-copy genes of varying length.
Conclusion: It is concluded that A2 sequences in *L. major* strains has homology with stage-specific S antigen-like protein (A2) of *L. major* and *L. donovani infantum*. A2 sequences in *L. tropica* strains have also homology with stage-specific S antigen-like protein (A2) of *L. major* and *L. tropica*.

PP-202 Fulminant liver failure in patient with leishmaniasis

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Introduction: Leishmaniasis is a disease which can be endemic, epidemic or sporadic. There are 88 countries in the world endemic of leishmaniasis, including Armenia. The clinical manifestation of leishmaniasis depends on the complex interaction of the parasites invasiveness, tropism and pathogenesity) and the host immune response.
The aim of this work is to show a rare case of visceral leishmaniasis in child.
Case description: Patient 1.5 years old, male, was emergency hospitalized in our clinic on the 20th day of illness with diagnosis of viral hepatitis. Clinical exam: prolonged fever, progressive weight loss, severe intoxication syndrome (weakness, anorexia, vomiting, nausea), expressed jaundice of the skin and mucous membrane, hepatosplenomegaly with predominantly enlarge of spleen.
Laboratory findings: HAV IgM, HBsAg, HBcor IgM, antiHCV are negative. Pancytopenia with HGB = 60g/dl, RBD = 1.8M/ul, WBC = 4.1; PLT = 60 k/ul; ESR 70. Biochemical analyses show increase of total bilirubin (534 μmol/l) with direct bilirubin (361.9 μmol/l); ALT = 3160 U/L, AST = 730 U/L, expressed dysproteinemia, PT 20%. US investigation demonstrated enlargement of liver and spleen with structure abnormalities, ascites.
Diagnosis of visceral leishmaniasis is based on clinical expressed symptoms and laboratory findings: isolation of *Leishmania donovani* through bone marrow aspirate culture, serological specific IgM positive.
The progression of the disease to fulminant liver failure with encephalopathy I–II° and ascites, was developed on the 4-th day of hospitalization. Result of complex therapy including etiological – meglumine antimoniate (glukantim) and pathogenetical treatment led to full recovery.

PP-203 *Taenia saginata* infection: a rare case of intestinal perforation from Northern Iran

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Background: Taeniasis is a worm infection known commonly in the North of Iran. It is caused by the beef tapeworm *Taenia saginata* and can lead to imperative situation surgical settings.